

**Query=** SEQ ID NO:43  
 (1650 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC018552.5.95189.106311	569	e-159
AC018552.5.17437.94328	<u>297</u>	1e-77

>AC018552.5.95189.106311  
 Length = 11123

Score = 569 bits (287), Expect = e-159  
 Identities = 287/287 (100%)  
 Strand = Plus / Plus

Query: 1257 atgctgggttcggtgaagggacaacccatgtacgccctctatatcacccgtccacggctactt 1316  
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 Sbjct: 5423 atgctgggttcggtgaagggacaacccatgtacgccctctatatcacccgtccacggctactt 5482

Query: 1317 cctcatcaccttcctcttttggcatggtggtcctggccctggtggtctggaagatcttcac 1376  
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 Sbjct: 5483 cctcatcaccttcctcttttggcatggtggtcctggccctggtggtctggaagatcttcac 5542

Query: 1377 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacccct 1436  
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 Sbjct: 5543 cctgtcccgtgctacagcgggtcaaggagcgggggaagaaccggaagaaggtgctcacccct 5602

Query: 1437 gctgggcctctcgagcctggtgggtgtgacatggggggtggccatcttcaccccggtggg 1496  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 5603 gctgggcctctcgagcctggtgggtgtgacatggggggtggccatcttcaccccggtggg 5662

Query: 1497 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 1543  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 5663 cctctccaccgtctacatctttgcacttttcaactccttgcaaggtg 5709

Score = 563 bits (284), Expect = e-157  
 Identities = 284/284 (100%)  
 Strand = Plus / Plus

Query: 880 aggcctttcccgaggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 939  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3710 aggcctttcccgaggagaggttcaagtcagaagatgccccaaagatccacgtggccctgggt 3769

Query: 940 ggcagcctgttcctcctgaatctggccttcttgggtcaatgtggggagtgggtcaaagggg 999  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 3770 ggcagcctgttcctcctgaatctggccttcttgggtcaatgtggggagtgggtcaaagggg 3829

Query: 1000 tctgatgctgcctgctgggcccgggggctgtcttccactacttcctgctctgtgccttc 1059  
|||||  
Sbjct: 3830 tctgatgctgcctgctgggcccgggggctgtcttccactacttcctgctctgtgccttc 3889

Query: 1060 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 1119  
|||||  
Sbjct: 3890 acctggatgggccttgaagccttccacctctacctgctcgctgtcagggctttcaacacc 3949

Query: 1120 tacttcgggcactacttcctgaagctgagcctggtgggctgggg 1163  
|||||  
Sbjct: 3950 tacttcgggcactacttcctgaagctgagcctggtgggctgggg 3993

Score = 228 bits (115), Expect = 9e-57  
Identities = 115/115 (100%)  
Strand = Plus / Plus

Query: 768 gagaccaccttggaccagtccacggtgcatacctcacacgcatctcccagggcgggctg 827  
|||||  
Sbjct: 284 gagaccaccttggaccagtccacggtgcatacctcacacgcatctcccagggcgggctg 343

Query: 828 tggggctctccatgatcttcctggccttcaccattattctttatgcctttctgagg 882  
|||||  
Sbjct: 344 tggggctctccatgatcttcctggccttcaccattattctttatgcctttctgagg 398

Score = 204 bits (103), Expect = 1e-49  
Identities = 103/103 (100%)  
Strand = Plus / Plus

Query: 1539 aggtgtcttcatctgctgctggttcaccatcctttacctccaagtcagagcaccacagt 1598  
|||||  
Sbjct: 8131 aggtgtcttcatctgctgctggttcaccatcctttacctccaagtcagagcaccacagt 8190

Query: 1599 ctctcctctactgcaagattggaccaggccactccgcatct 1641  
|||||  
Sbjct: 8191 ctctcctctactgcaagattggaccaggccactccgcatct 8233

Score = 204 bits (103), Expect = 1e-49  
Identities = 103/103 (100%)  
Strand = Plus / Plus

Query: 666 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 725  
|||||  
Sbjct: 43 agggaccactggagactggtcttctgagggctgctccacggaggtcagacctgaggggac 102

Query: 726 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 768  
|||||  
Sbjct: 103 cgtgtgctgctgtgaccacctgacctttttcgccctgctcctg 145

Score = 188 bits (95), Expect = 8e-45  
Identities = 95/95 (100%)  
Strand = Plus / Plus

Query: 1162 ggccctgcccgcctgatgggtcatcggcactgggagtgccaacagctacggcctctacacc 1221  
|||||  
Sbjct: 4169 ggccctgcccgcctgatgggtcatcggcactgggagtgccaacagctacggcctctacacc 4228

Query: 1222 atccgtgataggagaaccgcacctctctggagct 1256  
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Sbjct: 4229 atccgtgataggagaaccgcacctctctggagct 4263

>AC018552.5.17437.94328  
Length = 76892

Score = 297 bits (150), Expect = 1e-77  
Identities = 150/150 (100%)  
Strand = Plus / Plus

Query: 57 aggtcaggaaaagcccaccgaagggccaaagaaacacctgcctggggagcaacaacatgta 116  
|||||  
Sbjct: 68998 aggtcaggaaaagcccaccgaagggccaaagaaacacctgcctggggagcaacaacatgta 69057

Query: 117 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 176  
|||||  
Sbjct: 69058 cgacatcttcaacttgaatgacaaggctttgtgcttcaccaagtgcaggcagtcgggcag 69117

Query: 177 cgactcctgcaatgtggaaaacttgcagag 206  
|||||  
Sbjct: 69118 cgactcctgcaatgtggaaaacttgcagag 69147

Score = 297 bits (150), Expect = 1e-77  
Identities = 150/150 (100%)  
Strand = Plus / Plus

Query: 344 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttcca 403  
|||||  
Sbjct: 73847 aggttccgaggcaggtgatgaaggacgaggacaagccccctgacagagtgcgacttcca 73906

Query: 404 agagcctttttcgatccctgccaggcaacaggtctgtgggtccgcttggccgctcaccattc 463  
|||||  
Sbjct: 73907 agagcctttttcgatccctgccaggcaacaggtctgtgggtccgcttggccgctcaccattc 73966

Query: 464 tggacattgggtccagggactctcttcaagg 493  
|||||  
Sbjct: 73967 tggacattgggtccagggactctcttcaagg 73996

Score = 283 bits (143), Expect = 2e-73  
Identities = 143/143 (100%)  
Strand = Plus / Plus

Query: 205 agatactgggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 264  
|||||  
Sbjct: 71877 agatactgggctaaactacgaggcccatctgatgaaggaaggtttgacgcagaaggtgaac 71936

Query: 265 acgcctttcctgaaggctttgggtccagaacctcagcaccaaacactgcagaagacttctat 324  
|||||  
Sbjct: 71937 acgcctttcctgaaggctttgggtccagaacctcagcaccaaacactgcagaagacttctat 71996

Query: 325 ttctctctggagccctctcaggt 347  
|||||  
Sbjct: 71997 ttctctctggagccctctcaggt 72019

Score = 272 bits (137), Expect = 7e-70  
Identities = 141/142 (99%), Gaps = 1/142 (0%)  
Strand = Plus / Plus

Query: 487 ttca-agggtcccggtcggcctgggagatggcagcggtgtgaacaatcgctggt 545  
|||||  
Sbjct: 74849 ttcaagggtcccggtcggcctgggagatggcagcggtgtgaacaatcgctggt 74908

Query: 546 gggtttgagtgtgggacaaatgcatgtcaccaagctgggtgagcctctggagatcgtctt 605  
|||||  
Sbjct: 74909 gggtttgagtgtgggacaaatgcatgtcaccaagctgggtgagcctctggagatcgtctt 74968

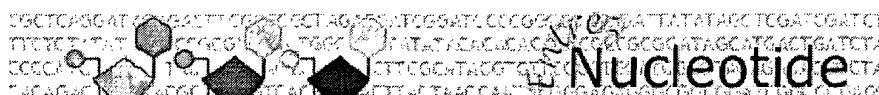
Query: 606 ctctcaccagcgaccgccccct 627  
|||||  
Sbjct: 74969 ctctcaccagcgaccgccccct 74990

Score = 119 bits (60), Expect = 6e-24  
Identities = 60/60 (100%)  
Strand = Plus / Plus

Query: 1 atggcgacgcccagggggcctggggggccctgctcctgctcctcctgctcccgacctcaggt 60  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 64026 atggcgacgcccagggggcctggggggccctgctcctgctcctcctgctcccgacctcaggt 64085

Score = 81.8 bits (41), Expect = 1e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 628 aacatgaccctcacctgtgtattctgggatgtgactaaagg 668  
||||||||||||||||||||||||||||||||||||||||  
Sbjct: 75495 aacatgaccctcacctgtgtattctgggatgtgactaaagg 75535



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Protein

Genome

Structure

PMC

Taxonomy

OMIM

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Limits

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Display

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☐ 1: AC018552. Homo sapiens chro...[gi:27476108]

Links

LOCUS AC018552 152156 bp DNA linear PRI 03-JAN-2003  
 DEFINITION Homo sapiens chromosome 16 clone RP11-405F3, complete sequence.  
 ACCESSION AC018552  
 VERSION AC018552.6 GI:27476108  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 152156)  
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los  
 Alamos National Laboratory.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 152156)  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-1999) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 REFERENCE 3 (bases 1 to 152156)  
 AUTHORS DOE Joint Genome Institute, Stanford Human Genome Center and Los  
 Alamos National Laboratory.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell  
 Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Jan 3, 2003 this sequence version replaced gi:13786352.  
 Draft Sequence Produced by DOE Joint Genome Institute  
 www.jgi.doe.gov  
 Finishing Completed at Stanford Human Genome Center and Los Alamos  
 National Laboratory  
 www-shgc.stanford.edu  
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